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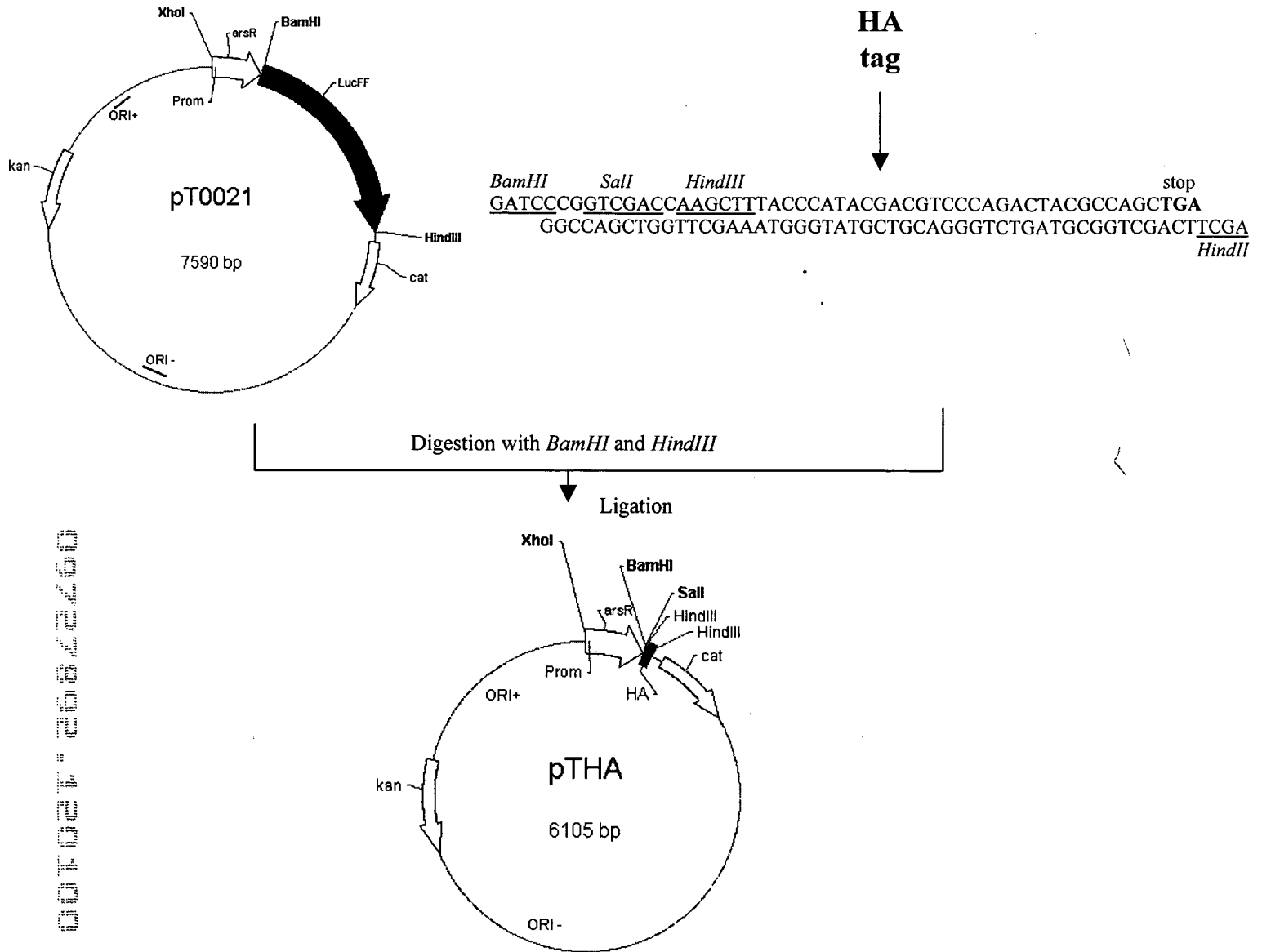
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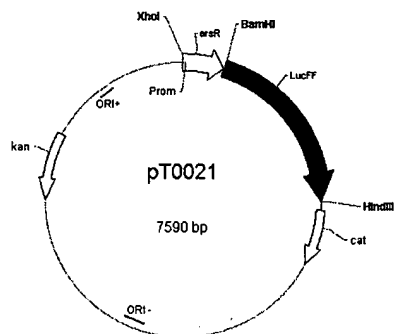
FIGURE 1A



B-

FIGURE 1B

PCR of pT0021 with XhoF and BamHNR



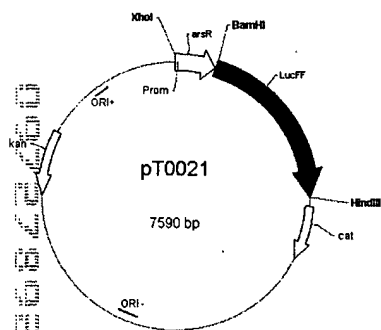
XhoF-5'-AATTCTCGAGTAAAATAACAT-3  
*XhoI*

AAATCAGGTGACTGTTGAGAAAAGGAGGCGGATCCCG-BamHNR  
Stop of *arsR* RBS *BamHI*

Digestion with *XhoI* and *BamHI*

Ligation

PCR of pT0021 with LucFFB and LucFFH



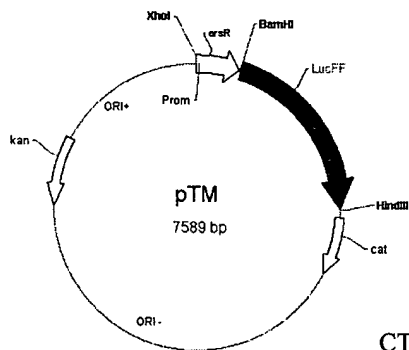
LucFFB-5'-CGGGATCCATGAGGGGTTCCGAAGACG  
*BamHI* Start of LucFF Original *BamHI* was modified

GAAAGTCCAAATTGTAAGCTTGGG-LucFFH  
Stop of *HindIII* LucFF

Digestion with *BamHI* and *HindIII*

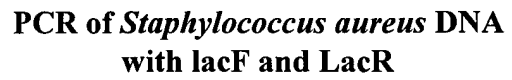
Ligation

Modified between stop of *arsR* to *BamHI*



- Modified in the vicinity of *BamHI*
- Cloning site for ORFs: *BamHI* and *HindIII*
- No additional codons in the induced protein

CTCGAG-----ATG-----TGAGAAAAGGAGGCGGATCCATG-----TAAGCTT  
*XhoI* Prom *arsR* RBS *BamHI* LucFF *HindIII*

[illegible]

GTAAAAGGAGTCTTATTGGATCCCG-LacR  
*Bam*HI

## Ligation

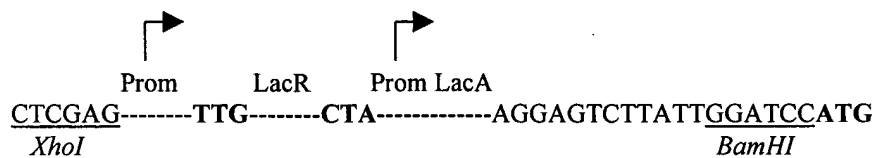


FIGURE 2A

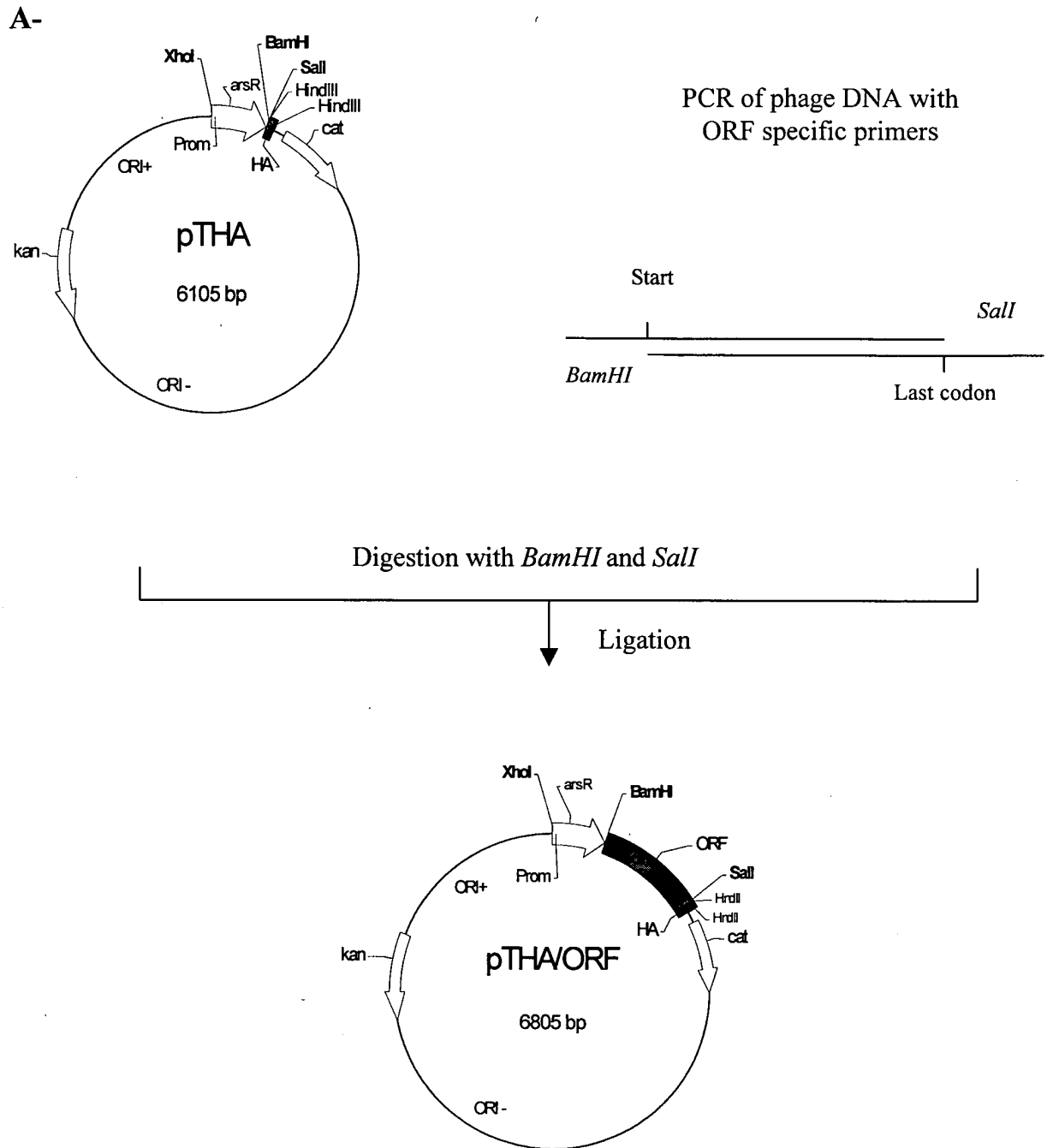


FIGURE 2B

B-

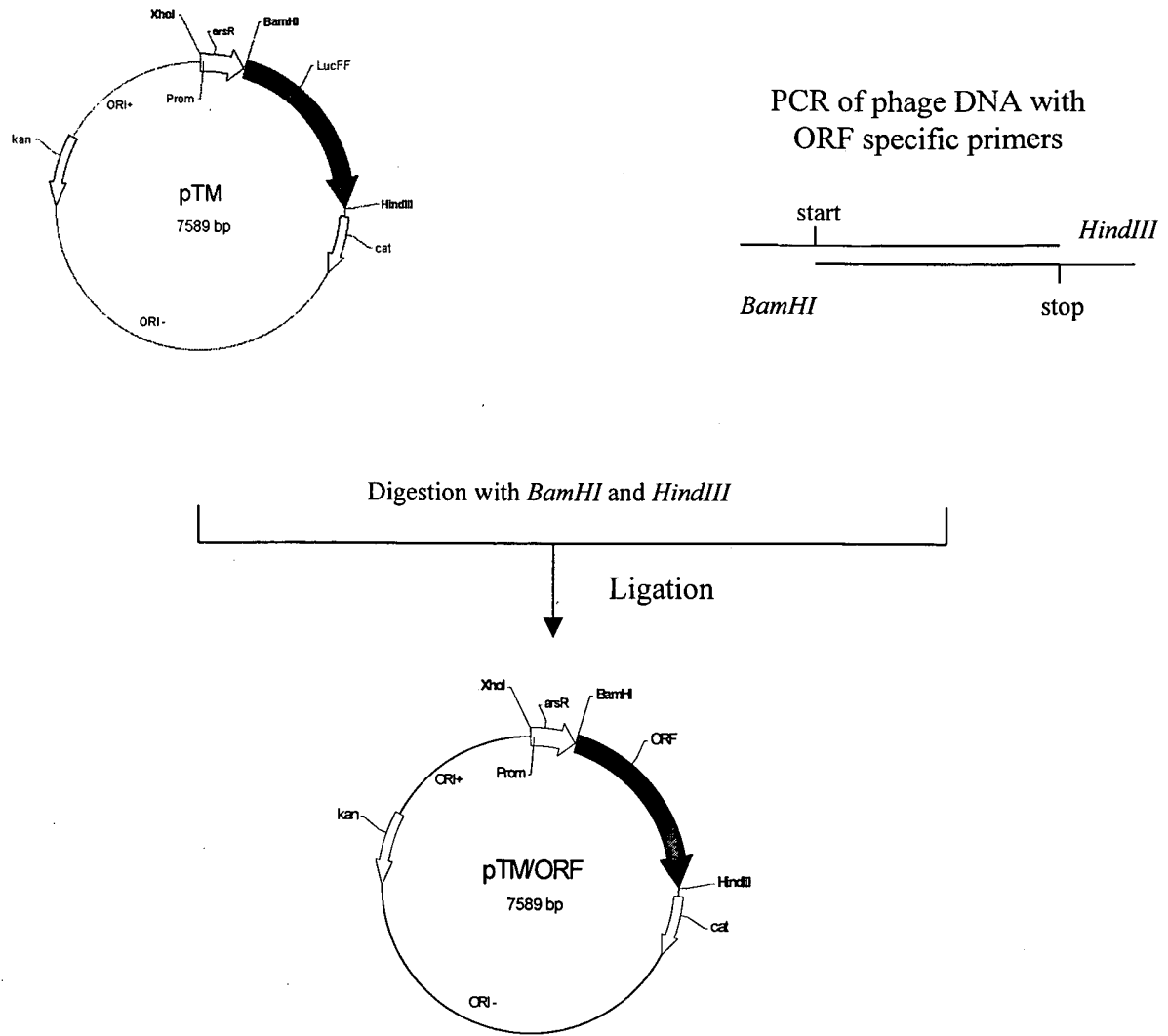
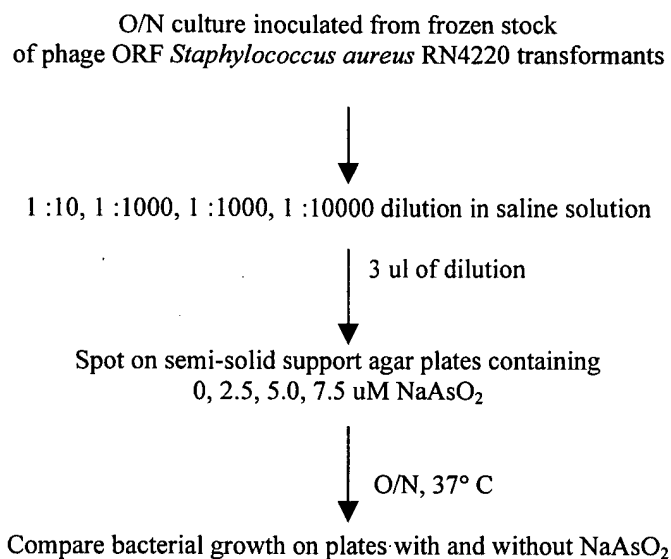


FIGURE 3

A) **Functional assay on semi-solid support medium**



B) **Functional assay in liquid medium**

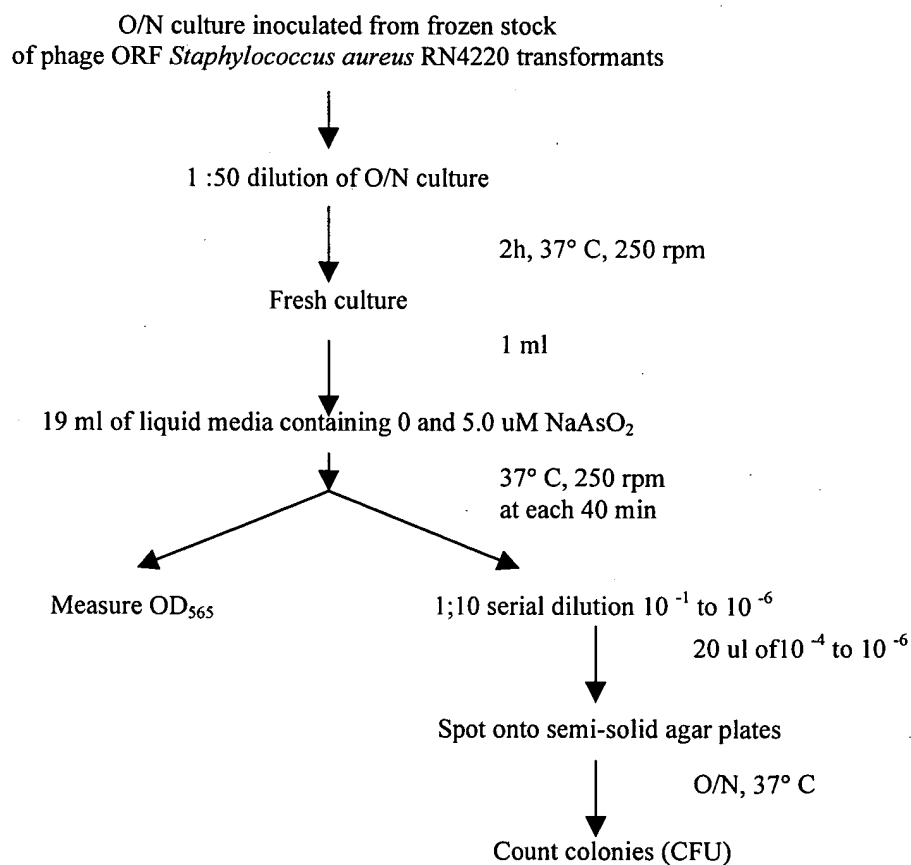


FIGURE 4A

A-

44AHJD ORFs tested for functional analysis

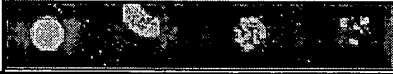

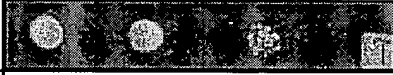
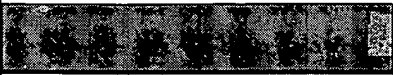
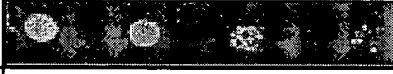
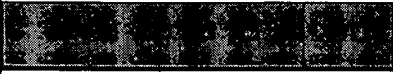







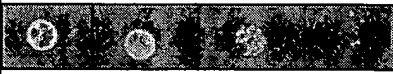
UID	POS
44AHJDORF001	12627..10342
44AHJDORF002	3789..5732
44AHJDORF003	6626..8389
44AHJDORF004	8764..10227
44AHJDORF005	13890..12643
44AHJDORF006	803..2029
44AHJDORF007	2044..3027
44AHJDORF008	3020..3775
44AHJDORF009	5744..6496
44AHJDORF010	14420..13938
44AHJDORF011	15593..15225
44AHJDORF012	8391..8813
44AHJDORF013	14996..14586
44AHJDORF019	9836..9630
44AHJDORF023	6494..6315
44AHJDORF025	15175..14999
44AHJDORF027	12916..13080
44AHJDORF028	9235..9071
44AHJDORF035	13957..13811
44AHJDORF036	10165..10019
44AHJDORF039	1743..1883
44AHJDORF040	9740..9877
44AHJDORF044	12917..12783
44AHJDORF046	4891..5019
44AHJDORF048	15340..15212
44AHJDORF049	5784..5909
44AHJDORF053	3348..3467
44AHJDORF113	199..600
44AHJDORF114	16172..15870
44AHJDORF121	16362..16165
44AHJDORF123	614..796

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FIGURE 4B

B-

ORF ID	<i>Staphylococcus aureus</i> transformants	Semi-solid support media		
		Without induction		With induction (5 uM sodium arsenite)
44AHJDORF12	Clone1			
	Clone2			
	Clone3			
44AHJDORF25	Clone1			
	Clone2			
	Clone3			
Control 77ORF30	Clone1			

001001"000000

FIGURE 5A

A-

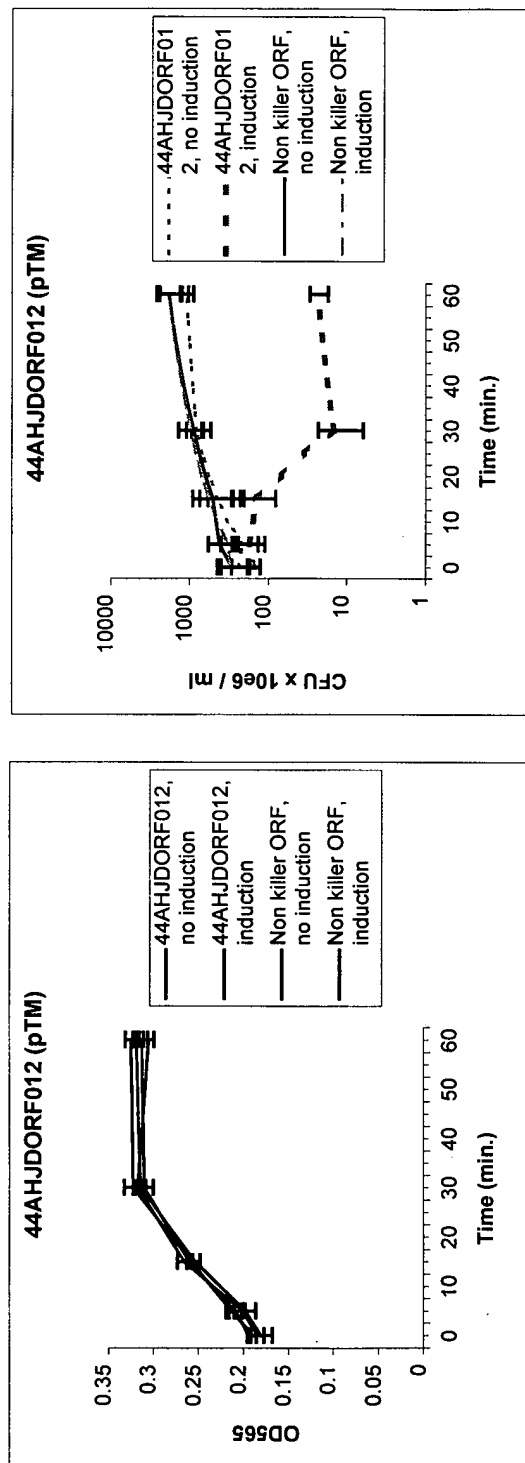
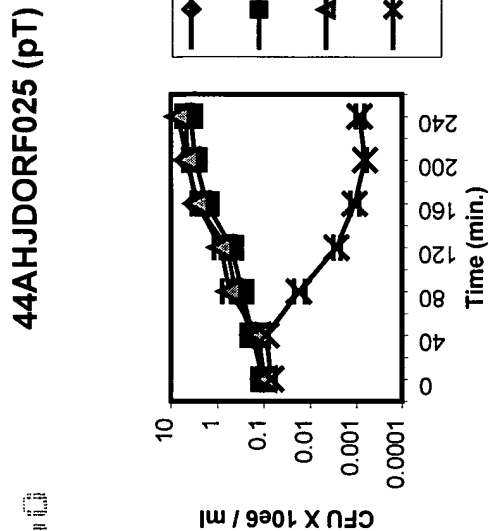
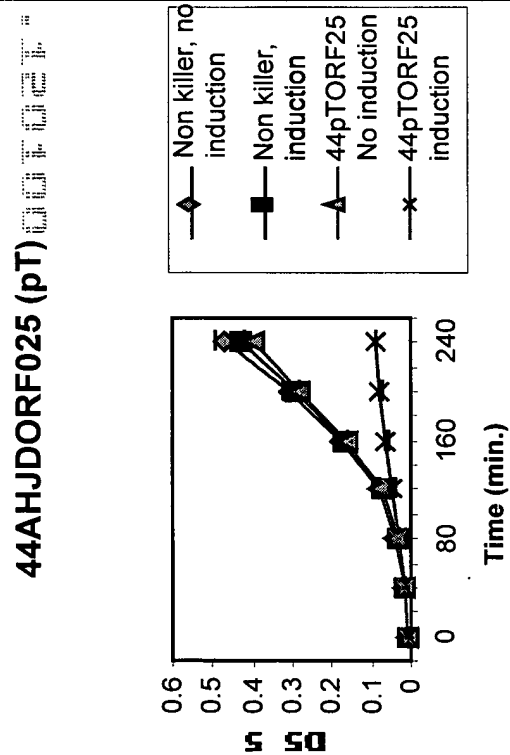
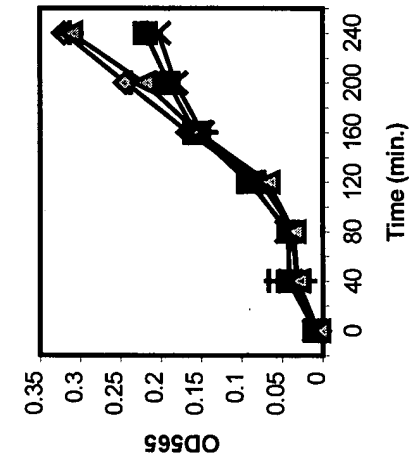


Fig  
.5B



### 44AHJD ORF 25 (pTMLac)



### 44AHJDORF25(pTMLac)

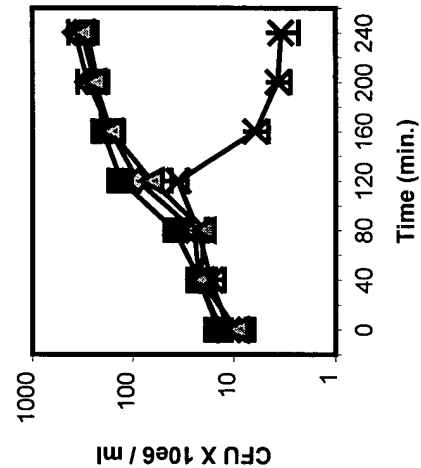
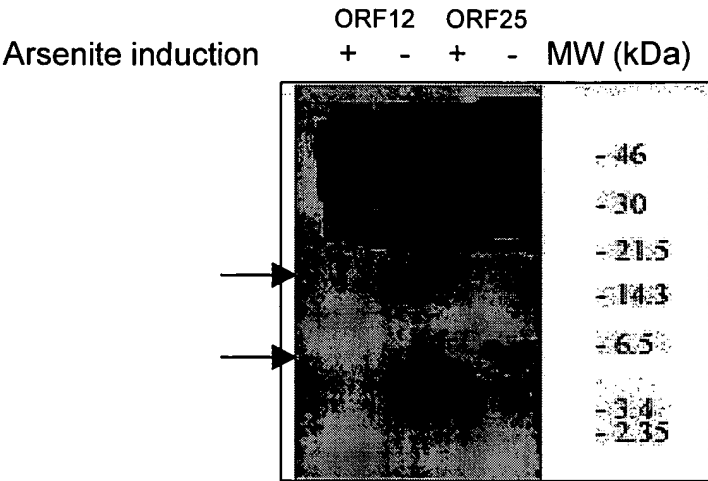
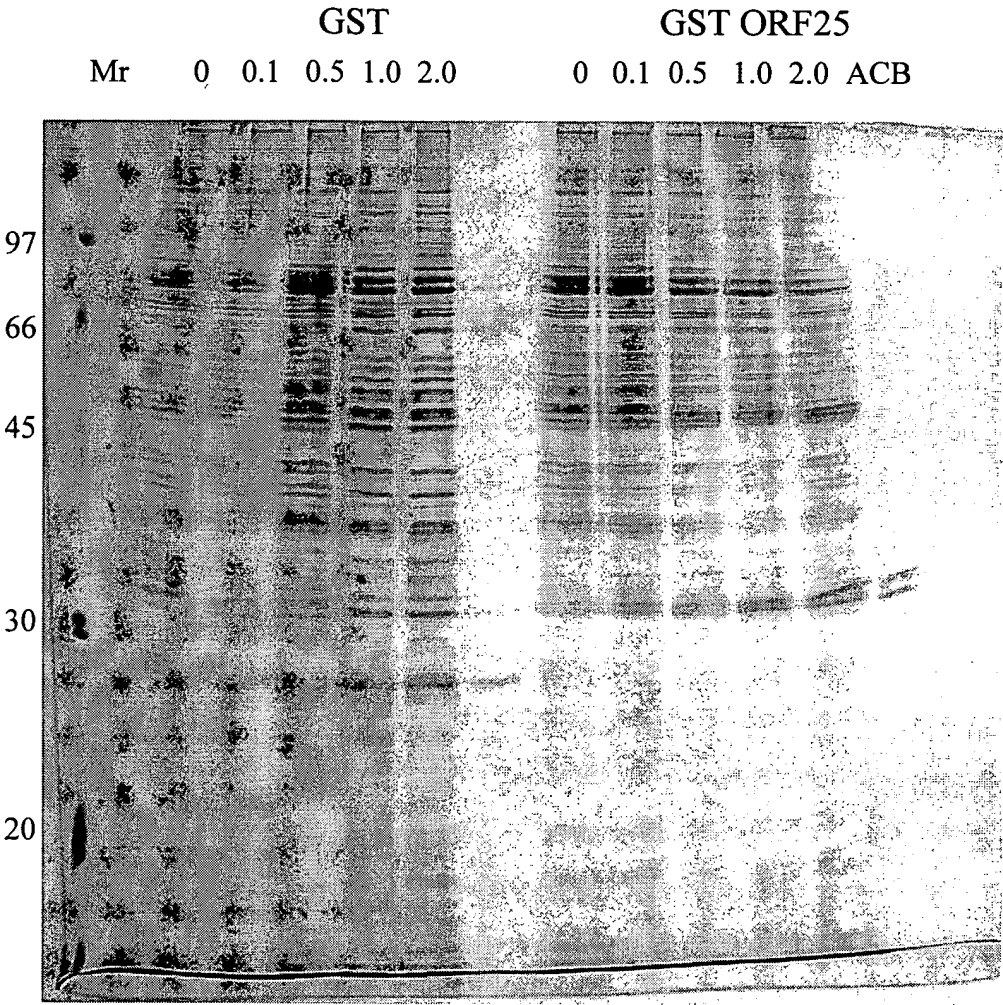


FIGURE 6



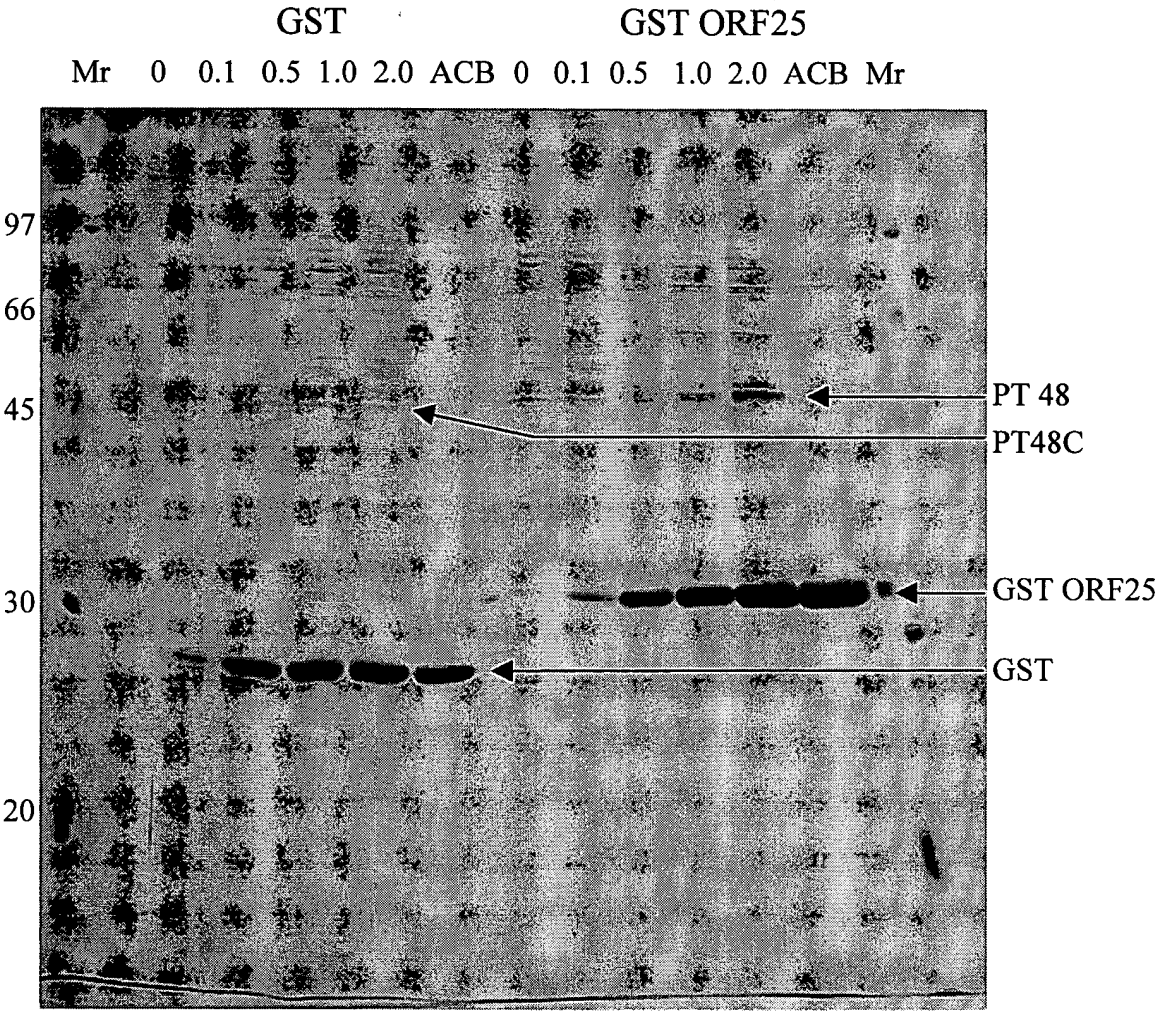
ORF12 = 263260

FIGURE 7A



001021-202403

FIGURE 7B

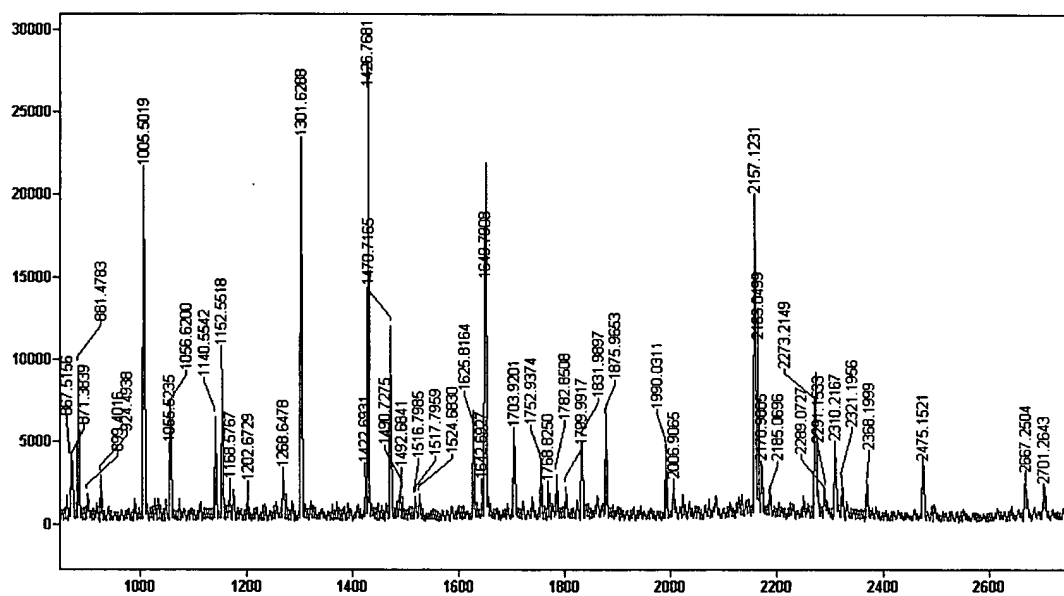


001021-268260

FIGURE 8

Tryptic peptide mass spectrum of 48 kDa interacting protein

(from Figure 1B)



# FIGURE 9

## Identification of PT48 as DNA-directed DNA polymerase III beta.

Details for: PT48

gi|1706496|sp|P50029|DP3B STAAU DNA POLYMERASE III BETA CHAIN

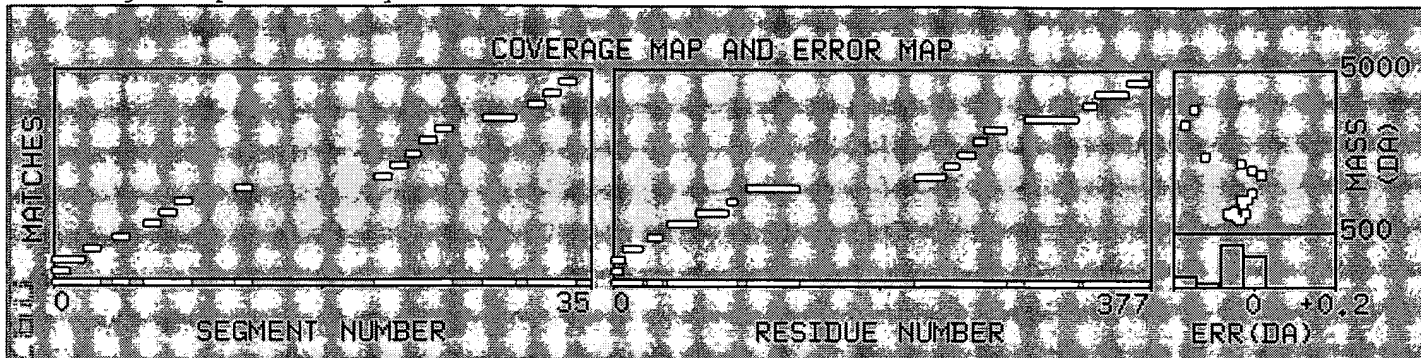
gi|1084187|pir|S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain - Staphylococcus aureus

Sample ID : PT 48

Number of Measured Peptides : 40

Number of Matched Peptides : 17

Coverage of protein sequence : 68%



Measured Mass(M)	Avg/ Mono	Computed Mass	Error (Da)	Residues Start To	Missed Cut	Peptide sequence
870.370	M	870.397	-0.027	333 339	0	YMMDALK
880.474	M	880.505	-0.032	82 88	0	FFVDIHK
898.392	M	898.429	-0.037	1 7	0	MMEFTIK
1004.492	M	1004.540	-0.048	235 243	0	VGNVNFISR
1054.514	M	1054.530	-0.016	1 8	1	MMEFTIKR
1055.603	M	1055.658	-0.055	26 35	0	TTLPILTGK
1151.546	M	1151.586	-0.040	255 263	0	LFPENYEIK
1300.619	M	1300.641	-0.021	244 254	0	LLEGHYPDTR
1425.769	M	1425.782	-0.013	363 375	0	GDDSVTQLLPIR
1469.713	M	1469.740	-0.026	9 20	0	DYFITQLNDTLK
1648.781	M	1648.784	-0.003	264 277	0	LSTDNGEFYHADR
2156.112	M	2156.095	0.017	61 81	0	TVDGEDIVNISETGSVVLPR
2309.198	M	2309.199	-0.000	40 60	0	EHEVILTGSDSEISIEITPK
2474.139	M	2474.166	-0.027	214 234	0	IMSDNEEDIDIFFASNOVLEK
2666.266	M	2666.365	-0.099	340 362	0	AIDNDEVEVEFFGTMPFLKPK
3577.670	A	3577.809	-0.139	292 326	1	LSTGDDVVELSSTSPKIGTVKEEVDANDVEGGSLK
4033.298	A	4033.421	-0.123	97 132	0	LSTNEOFOTLITSGHSEFNLSGLDPDOYPLLPOVSR



## FIGURE 10

### SEQ ID NO : 1 *Staphylococcus aureus* DnaN nucleotide sequence

ATGATGGAATTCACTATTAAAGAGATTATTTTATTACACAATTAAATGACACATTAAAA  
GCTATTTACCAAGAACAACATTACCTATATTAACGGTATCAAAATCGATGCGAAAGAA  
CATGAAGTTATATTAACGGTTCAGACTCTGAAATTTCAATAGAAATCACTATTCCTAAA  
ACTGTAGATGGCGAAGATATTGTCAATATTTAGAAACAGGCTCAGTAGTACTTCCTGGA  
CGATTCTTTGTTGATATTATAAAAAAATTACCTGGTAAAGATGTTAAATTATCTACAAAT  
GAACAATTCCAGACATTAATTACATCAGGTCATTCTGAATTTAATTTAAGTGGCTTAGAT  
CCAGATCAATATCCTTTATTACCTCAAGTTTCTAGAGATGACGCAATTCAATTGTCGGTA  
AAAGTGCTTAAAAACGTGATTGCACAAACAAATTTTGCAGTGTCCACCTCAGAAACACGC  
CCAGTACTAACTGGTGTGAACTGGCTTATACAAGAAAATGAATTAATATGCACAGCGACT  
GACTCACACCGCTTGGCTGTAAGAAAGTTGCAGTTAGAAGATGTTTCTGAAAACAAAAAT  
GTCATCATTCCAGGTAAGGCTTTAGCTGAATTAATAAAATTATGTCTGACAATGAAGAA  
GACATTGATATCTTCTTTGCTTCAAACCAAGTTTATTTAAAGTTGGAAATGTGAACTTT  
ATTTCTCGATTATTAGAAGGACATTATCCTGATACAACACGTTTATTCCCTGAAAACAT  
GAAATTAATTAAGTATAGACAATGGGGAGTTTATCATGCGATTGATCGTGCCTCTTTA  
TTAGCGCGTGAAGGTGGTAATAACGTTATTAAATTAAGTACAGGTGATGACGTTGTTGAA  
TTGCTTCTACATCACCAGAAATTGGTACTGTAAAAGAAGAAGTTGATGCAAACGATGTT  
GAAGGTGGTAGCCTGAAAATTTCAATCACTCTAAATATATGATGGATGCTTTAAAAGCA  
ATCGATAATGATGAGGTTGAAGTTGAATTCTTCGGTACAATGAAACCATTATTTCTAAAA  
CCAAAAGGTGACGACTCGGTAACGCAATTAATTTTACCAATCAGAACTTACTAA

### SEQ ID NO : 2 *Staphylococcus aureus* DnaN amino acid sequence

>gi|1084187|pir|S54708 DNA-directed DNA polymerase (EC 2.7.7.7) III beta chain -  
*Staphylococcus aureus*

MMEFTIKRDYFITQLNDTLKAISPRITLPILTGKIDAKEHEVILTGSDSEISIEITIPKTVDGEDIVNI  
SETGSVVLPGRRFFVDIIKKLPKGDVKLSTNEQFQTLITSGHSEFNLSGLDPDQYPLLPQVSRDDAIQLSV  
KVLKNVIAQTNFAVSTSETRPVLTVGNWLIQENELICTATDSHRLAVRKLQLEDVSENKNV IIPGKALAE  
LNKIMSDNEEDIDIFFASNQVLFKVGNNVFISRLLEGHPDTRLFPENYEIKLSIDNGEFYHAIDRASL  
LAREGGNNVIKLSTGDDVVELSSTSPEIGTVKEEVDANDVEGSLKISFNSKYMMDALKAIDNDEVEVEF  
FGTMKPFILKPKGDDSVTQLILPIRTY